

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 15:16:35 ; Search time 7.58967 Seconds
(without alignments)
2484.756 Million cell updates/sec

Title: US-09-272-809-9

Perfect score: 1024

Sequence: 1 KLAVRAISRQLSPGGDIGA.....QAFGLQWELQASLAEX 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024	100.0	1112	2 S46313	phytochrome E - Ar
2	840.5	82.1	1131	2 T09701	phytochrome - Scot
3	836	81.6	1135	2 T16973	phytochrome B - cu
4	828	80.9	1132	2 T03668	phytochrome B - co
5	806	78.7	1039	2 T14802	phytochrome B - so
6	802.5	78.4	1172	1 FKMUB	phytochrome B - Ar
7	794.5	77.6	1171	2 S14085	phytochrome B - ri
8	785	76.7	1142	2 S62714	phytochrome 1b - M
9	783	76.5	1164	2 B71429	phytochrome D - Ar
10	772	75.4	1156	2 T07756	phytochrome B - so
11	765.5	74.8	1136	2 T14842	phytochrome - Norw
12	763.5	74.6	577	2 S58130	phytochrome - moss
13	763.5	74.6	1129	2 S28431	phytochrome B - po
14	747	72.9	1134	2 S31280	phytochrome - Mart
15	746	72.9	368	2 T09496	phytochrome - Doug
16	740.5	72.3	1132	2 S37206	phytochrome - moss
17	734.5	71.7	1135	2 T14803	phytochrome C - so
18	723.5	70.7	1303	1 S27396	phytochrome / prot
19	717.5	70.1	211	2 S62720	phytochrome B1 - S
20	707	69.0	210	2 S62721	phytochrome B2 - S
21	706	68.9	1111	1 FKMUC	phytochrome C - Ar
22	687	67.1	1465	2 T30891	PHY3 protein - mai
23	672	65.6	1122	1 FKMUA	phytochrome A - Ar
24	672	65.6	1122	2 D86229	phytochrome A [imp
25	671.5	65.6	1123	2 S20497	phytochrome A - po
26	669.5	65.4	1129	2 A29631	phytochrome 3 - oa
27	668.5	65.3	495	2 S00098	phytochrome 5 - oa
28	668	65.2	1129	2 S2631	phytochrome A - pa
29	666.5	65.1	1129	2 S00097	phytochrome 4 - oa

30 666 65.0 1124 1 FKPUZ phytochrome - zucc
31 665.5 65.0 1124 2 S06856 phytochrome (clone
32 665.5 65.0 1128 2 S03728 phytochrome A - po
33 662.5 64.7 1125 2 T09835 phytochrome A - ma
34 660.5 64.5 1131 2 JQ0382 phytochrome A - so
35 646 63.1 1131 2 T07137 phytochrome A - so
36 584.5 57.1 190 2 S46926 phytochrome 2 - No
37 561 54.8 156 2 T14837 phytochrome - Nym
38 548 53.5 189 2 S46927 phytochrome - Char
39 521 50.9 197 2 S46928 phytochrome 3 - No
40 513 50.1 156 2 T14838 phytochrome - Norw
41 507.5 49.6 314 2 T14865 phytochrome 4 - No
42 501 48.9 156 2 T14839 phytochrome - Norw
43 489 47.8 156 2 T14836 phytochrome E - ga
44 474 46.3 105 2 T17026 phytochrome - Doug
45 455.5 44.5 115 2 T09337

ALIGNMENTS

RESULT 1

S46313

Phytochrome E - Arabidopsis thaliana

N/Alternate names: protein F15J5.100

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 31-Dec-2004

C/Accession: S46313; T14813; S41912

R/Clack, T.; Mathews, S.; Sharrock, R.A.

Plant Mol. Biol. 25, 413-427, 1994

A/Title: The phytochrome apoprotein family in Arabidopsis is encoded by five genes: the

A/Reference number: S46312; MUID:94325466; PMID:8049367

A/Accession: S46313

A/Molecule type: DNA

A/Residues: 1-1112 <CLA>

A/Cross-references: UNIPROT:P42498; UNIPARC:UPI0000131A6B; EMBL:X76610; NID:G452815; PID:

R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.F.

submitted to the Protein Sequence Database, August 1999

A/Reference number: Z18120

A/Accession: T14813

A/Molecule type: DNA

A/Residues: 1-1112 <BEV>

A/Cross-references: UNIPARC:UPI0000131A6B; EMBL:AL110123; GSPDB:GN00062; ATSP:F15J5.100

A/Experimental source: cultivar Columbia; BAC clone F15J5

C/Genetics:

A/Gene: PHYE; ATSP:F15J5.100

A/Map position: 4

A/Introns: 665/1; 934/2; 1032/2

C/Superfamily: phytochrome, conventional type; phytochrome homology

C/Keywords: chromoprotein; photoreceptor; phytochromobilin

F/63-569/Domain: phytochrome homology <PHYT>

F/322/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 100.0%; Score 1024; DB 2; Length 1112;

Best Local Similarity 100.0%; Pred. No. 5.5e-93;

Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLAVRAISRQLSPGGDIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVVSIRSDL 60

Db 201 KLAVRAISRQLSPGGDIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVVSIRSDL 260

Qy 61 EPYLGILHYPATDIPQAAARFLFKQNRVRMIDCNATPVKVYQVSEELKPLCLVNSTLRAPH 120

Db 261 EPYLGILHYPATDIPQAAARFLFKQNRVRMIDCNATPVKVYQVSEELKPLCLVNSTLRAPH 320

Qy 121 GCHTQYNNMGVSVASLALAIWVGKSSKLWGLVVGHCSPRYVPFFPLRYACEFLMQAFG 180

Db 321 GCHTQYNNMGVSVASLALAIWVGKSSKLWGLVVGHCSPRYVPFFPLRYACEFLMQAFG 380

Qy 181 LQLQWELQASLAEX 196

Db 381 LQLQWELQASLAEX 396

RESULT 2
T09701
phytochrome - Scotch pine
C;Species: Pinus sylvestris (Scotch pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C;Accession: T09701
R;Wiegmann-Ehrund, C.M.; Kolukisaoglu, H.U.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z16826
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-1131 <WIE>
A;Cross-references: UNIPROT:Q41046; UNIPARC:UPI0000131A71; EMBL:X96738; NID:g1237083
A;Experimental source: isolate PSA 5.1
C;Superfamily: phytochrome, conventional type; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;75-587/Domain: phytochrome homology <PHY>
F;332/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 82.1%; Score 840.5; DB 2; Length 1131;
Best Local Similarity 78.0%; Pred. No. 8.3e-75;
Matches 160; Conservative 15; Mismatches 21; Indels 9; Gaps 1;

QY 1 KLAVRAISRLOSLPGDIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVSEIRSDL 60
Db 211 KLAVRAISRLOSLPGDVGGLCDTVVENVRELTYGDRVMVYKFHEDHGEVVAEIRSDL 270

QY 61 EPYLGLHYPATDIPQARFLFKQNRVIMCDNCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
Db 271 EPYLGLHYPATDIPQARSLFLFQNRVIMCDNCNATPVKIQSELMQPLCLVNSTLRAPH 330

QY 121 GCHTOYMANNGSVASIALAIVVKGKD-----SSKLMLVGVGHCHSPRYVPFPLRYAC 171
Db 331 GCHAOYMANNGSVASIALAIVVKGKD-----SSKLMLVGVGHCHSPRYVPFPLRYAC 390

QY 172 CEFMLQAFGLQLOMELQASOLAELK 196
Db 391 CEFMLQAFGLQLOMELQASOLAELK 415

RESULT 3
T16973
phytochrome B - curled-leaved tobacco
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T16973
R;Hudson, M.E.; Robson, P.R.H.; Kraepiel, Y.; Caboche, M.; Smith, H.
Plant J. 12, 1091-2101, 1997
A;Title: Nicotiana plumbaginifolia hlg mutants have a mutation in a PHYB-type phytochrome
A;Reference number: Z18626; MUID:98079245; PMID:9418050
A;Accession: T16973
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-1135 <HJD>
A;Cross-references: UNIPROT:O24117; UNIPARC:UPI000000A9556; EMBL:Y14676; NID:g2370330; PI
A;Experimental source: cultivar PBH1d; leaf
C;Genetics:
A;Gene: PHYB
C;Superfamily: phytochrome, conventional type; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;82-592/Domain: phytochrome homology <PHY>
F;338/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 81.6%; Score 836; DB 2; Length 1135;
Best Local Similarity 77.0%; Pred. No. 2.3e-74;
Matches 157; Conservative 18; Mismatches 21; Indels 8; Gaps 1;

QY 1 KLAVRAISRLOSLPGDIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVSEIRSDL 60
Db 217 KLAVRAISRLOSLPGDVGKILCDTVVESVRELTYGDRVMVYKFHEDHGEVVAESKRPD 276

QY 61 EPYLGLHYPATDIPQARFLFKQNRVIMCDNCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
Db 277 EPYLGLHYPATDIPQARSLFLFKQNRVIMCDNCNATPVKVVQSELMQPLCLVNSTLRAPH 336

QY 121 GCHTOYMANNGSVASIALAIVVKGKD-----SSKLMLVGVGHCHSPRYVPFPLRYAC 172
Db 337 GCHAOYMANNGSVASIALAIVVKGKD-----SSKLMLVGVGHCHSPRYVPFPLRYAC 396

QY 173 EFLMQAFGLQLOMELQASOLAELK 196
Db 397 EFLMQAFGLQLOMELQASOLAELK 420

RESULT 4
T03668
phytochrome B - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T03668; T03672
R;Kern, R.; Gasch, A.; Deak, M.; Kay, S.A.; Chua, N.H.
Plant Physiol. 102, 1363-1364, 1993
A;Title: PhyB of tobacco, a new member of the photoreceptor family.
A;Reference number: Z14996; MUID:94105358; PMID:8278560
A;Accession: T03668
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1132 <KER>
A;Cross-references: UNIPROT:P29130; UNIPARC:UPI0000131A67; EMBL:L10114; NID:g295345; PIDN
R;Lopez-Juez, E.; Nagatani, A.; Tomizawa, K.; Deak, M.; Kern, R.; Kendrick, R.E.; Furuya,
Plant Cell 4, 241-251, 1992
A;Title: The cucumber long hypocotyl mutant lacks a light-stable PHYB-like phytochrome.
A;Reference number: Z14997; MUID:92361250; PMID:1498594
A;Accession: T03672
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 457-506, 'S', 508-586, 'Q', 587-1132 <LOP>
A;Cross-references: UNIPARC:UPI000016DB89; EMBL:M65023; NID:g170286; PIDN:AAA34093.1; PI
C;Genetics:
A;Gene: phyB
C;Superfamily: phytochrome, conventional type; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;80-589/Domain: phytochrome homology <PHY>
F;336/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 80.9%; Score 828; DB 2; Length 1132;
Best Local Similarity 76.5%; Pred. No. 1.4e-73;
Matches 156; Conservative 18; Mismatches 22; Indels 8; Gaps 1;

QY 1 KLAVRAISRLOSLPGDIGALCDTVVEDVQRLTGDRVMVYQFHEDDHGEVSEIRSDL 60
Db 215 KLAVRAISRLOSLPGDVGKLLCDTVVESVRELTYGDRVMVYKFHEDHGEVVAESKIPDL 274

QY 61 EPYLGLHYPATDIPQARFLFKQNRVIMCDNCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
Db 275 EPYLGLHYPATDIPQARSLFLFKQNRVIMCDNCNATPVKVVQSELMQPLCLVNSTLRAPH 334

QY 121 GCHTOYMANNGSVASIALAIVVKGKD-----SSKLMLVGVGHCHSPRYVPFPLRYAC 172
Db 335 GCHAOYMANNGSVASIALAIVVKGKD-----SSKLMLVGVGHCHSPRYVPFPLRYAC 394

QY 173 EFLMQAFGLQLOMELQASOLAELK 196
Db 395 EFLMQAFGLQLOMELQASOLAELK 418

RESULT 5
T14802
phytochrome B - sorghum (fragment)
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T14802
R;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet,

S62714
phytochrome 1b - Mesotaenium caldariorum
C:Species: Mesotaenium caldariorum
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C:Accession: S62714
R:Lagaras, D.M.; Wu, S.H.; Lagarias, J.C.
Plant Mol. Biol. 29, 1127-1142, 1995
A:Title: Atypical phytochrome gene structure in the green alga Mesotaenium caldariorum.
A:Reference number: S62713; MUID:96191280; PMID:8616213
A:Accession: S62714
A:Molecule type: DNA
A:Residues: 1-1142 <LAG>
A:Cross-references: UNIPROT:Q40263; UNIPARC:UPI000009D253; EMBL:U31284; NID:g1125698; PIDN
C:Genetics:
A:Introns: 125/1; 298/3; 393/3; 468/3; 543/2; 621/3; 699/1; 785/1; 856/3; 970/2; 1067/2
C:Superfamily: phytochrome, conventional type; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
F:68-589/Domain: phytochrome homology <PHYT>
F:880-1139/Domain: signal transduction #status predicted <STD>
F:324/Binding site: phytochromobilin (Cys) (covalent) #status predicted
Query Match 76.7%; Score 785; DB 2; Length 1142;
Best Local Similarity 70.0%; Pred. No. 2.6e-69;
Matches 147; Conservative 20; Mismatches 29; Indels 14; Gaps 1;
QY 1 KLAVRAISRLQSLPGGDIGALCDTVVVDVORLTGYDRVMVYQFHHDDHGEVSEIRRSDL 60
DB 203 KLAARISRLQSLPGGDIGALCDTVVVDVORLTGYDRVMVYQFHHDDHGEVSEIRRSDL 262
QY 61 EPYLGLHYPATDIPQAAFLFKQNRVMI CDCNATPVKVQSEELKRPCLCLVNSTLRAPH 120
DB 263 EPYLGLHYPATDIPQAAFLFKQNRVMI CDCNATPVKVQSEELKRPCLCLVNSTLRAPH 322
QY 121 GCHTQYMANNGSVASLALAIIVKQSS-----KLWGLVGHCHSPRYVPF 166
DB 323 GCHTQYMANNGSVASLALAIIVKQSS-----KLWGLVGHCHSPRYVPF 382
QY 167 PLRYACEFLMQAFGLQLOMELQASLAQAEK 196
DB 383 PLRYACEFLMQAFGLQLOMELQASLAQAEK 412
RESULT 9
B71429
phytochrome D - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 31-Dec-2004
C:Accession: B71429; S46312; S41910
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dick
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzengger, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moeres, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha
A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: B71429
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1164 <BEV>
A:Cross-references: UNIPROT:P42497; UNIPARC:UPI0000131A6A; GB:Z57340; NID:g2244950; PIDN
R:Clack, T.; Mathews, S.; Sharrock, R.A.
Plant Mol. Biol. 25, 413-427, 1994
A:Title: The phytochrome apoprotein family in Arabidopsis is encoded by five genes: the
A:Reference number: S46312; MUID:94325466; PMID:8049367
A:Accession: S46312
A:Molecule type: DNA
A:Residues: 1-424, 'F', 426-1164 <CLA>
A:Cross-references: UNIPARC:UPI000016DBB1; EMBL:X76609; NID:g452812; PIDN:CAA54072.1; PI
C:Genetics:
A:Gene: PHYD

A:Map position: 4COP9-4G3845
C:Superfamily: phytochrome, conventional type; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
F:103-618/Domain: phytochrome homology <PHYT>
F:360/Binding site: phytochromobilin (Cys) (covalent) #status predicted
Query Match 76.5%; Score 783; DB 2; Length 1164;
Best Local Similarity 71.2%; Pred. No. 4.3e-69;
Matches 148; Conservative 24; Mismatches 24; Indels 12; Gaps 1;
QY 1 KLAVRAISRLQSLPGGDIGALCDTVVVDVORLTGYDRVMVYQFHHDDHGEVSEIRRSDL 60
DB 239 KLAARISRLQSLPGGDIGALCDTVVVDVORLTGYDRVMVYQFHHDDHGEVSEIRRSDL 298
QY 61 EPYLGLHYPATDIPQAAFLFKQNRVMI CDCNATPVKVQSEELKRPCLCLVNSTLRAPH 120
DB 299 EPYLGLHYPATDIPQAAFLFKQNRVMI CDCNATPVKVQSEELKRPCLCLVNSTLRAPH 358
QY 121 GCHTQYMANNGSVASLALAIIVK-----GKSSKLWGLVGHCHSPRYVPFPL 168
DB 359 GCHTQYMANNGSVASLALAIIVK-----GKSSKLWGLVGHCHSPRYVPFPL 418
QY 169 RYACEFLMQAFGLQLOMELQASLAQAEK 196
DB 419 RYACEFLMQAFGLQLOMELQASLAQAEK 446
RESULT 10
T07756
phytochrome B - soybean
C:Species: Glycine max (soybean)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 31-Dec-2004
C:Accession: T07756
R:Rahn, T.R.; Woo, T.W.; Seo, H.S.; Choi, Y.D.
submitted to the EMBL Data Library, July 1994
A:Description: Nucleotide sequence of phytochrome B gene from Soybean (Glycine max L.).
A:Reference number: Z16118
A:Accession: T07756
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1156 <HAH>
A:Cross-references: UNIPROT:P42499; UNIPARC:UPI0000131A66; EMBL:L34843; NID:g516102; PIDN
A:Experimental source: strain Paidal; leaf seedling
C:Genetics:
A:Gene: phyB
A:Introns: 712/1; 810/3; 987/2; 1085/2
C:Superfamily: phytochrome, conventional type; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin
F:82-612/Domain: phytochrome homology <PHY>
F:358/Binding site: phytochromobilin (Cys) (covalent) #status predicted
Query Match 75.4%; Score 772; DB 2; Length 1156;
Best Local Similarity 72.6%; Pred. No. 5.2e-68;
Matches 146; Conservative 20; Mismatches 27; Indels 8; Gaps 1;
QY 4 VRAISRLQSLPGGDIGALCDTVVVDVORLTGYDRVMVYQFHHDDHGEVSEIRRSDL 63
DB 240 VRAISRLQSLPGADVKLLCDTVVSVRELTGYDRVMVYQFHHDDHGEVSEIRRSDL 299
QY 64 IGLHYPATDIPQAAFLFKQNRVMI CDCNATPVKVQSEELKRPCLCLVNSTLRAPHGCH 123
DB 300 IGLHYPATDIPQAAFLFKQNRVMI CDCNATPVKVQSEELKRPCLCLVNSTLRAPHGCH 359
QY 124 TQYMANNGSVASLALAIIVKGD-----SSKLWGLVGHCHSPRYVPFPLRYACEFL 175
DB 360 AQYMANNGSVASLALAIIVKGD-----SSKLWGLVGHCHSPRYVPFPLRYACEFL 419
QY 176 MQAFGLQLOMELQASLAQAEK 196
DB 420 MQAFGLQLOMELQASLAQAEK 440
RESULT 11

Db 318 GCCTAAGTGGGCTAGTAAVAVIINDNEEDSRGAIQGRKGLVGVCHTSPRTVPFPPLRSA 377
QY 172 CEFLMQAFGLQLOMELQLASQLAEK 196
Db 378 CEFLMQVFGQLNNEVELAAQLREK 402

RESULT 13
S28431
phytochrome B - potato
C:Species: Solanum tuberosum (potato)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 31-Dec-2004
C:Accession: S28431
R:Heyer, A.; Gatz, C.
Plant Mol. Biol. 20, 589-600, 1992
A:Title: Isolation and characterization of a cDNA-clone coding for potato type
A:Reference number: S28431; MUID:93081720; PMID:1450376
A:Accession: S28431
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1129 <HEY>
A:Cross-references: UNIPROT:P34094; UNIPARC:UPI0000131A64; GB:S51538; NID:g2612
C:Genetics:
A:Gene: phyB
C:Superfamily: phytochrome, conventional type; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regul
F:76-598/Domain: phytochrome homology <PHYT>
F:333/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 74.6%; Score 763.5; DB 2; Length 1129;
Best Local Similarity 74.7%; Pred. No. 3.5e-67;
Matches 142; Conservative 18; Mismatches 21; Indels 9; Gaps 1;
QY 16 GDTCALCDTVEDVQRLTGTVDRVMVYQFHEDDHGEVVSSETRRSDLPEVLGLHYEPTDIPQ 75
Db 227 GTUKLCDTVESRELTGTVDRVMVYKFDEHGEVVAESKRSOLEPYIGLHYEPTDIPQ 286

QY 76 AARFLFKQNRVRMICDNATPVKVQVSEELKRPCLCLVNSTLRAPHGCHTQYMANMGSVAS 135
Db 287 ASRFLFKQNRVRMIVCHATPVRTQDSLMLQPLCLVGLSTLRAPHGCHTQYMANMGSIAS 346

QY 136 LALAIVVVGKD-----SSKWLGLVGVGHGCSPRVPPPLRYACBFLMQAFGLQLOME 186
Db 347 LTLAVIINGNDEAVGGGRNSMELGLVGVGHGHTSVRSIPPLRYACBFLMQAFGLQLNME 406

QY 187 LQASQLAEK 196
Db 407 LQASQLSEK 416

RESULT 14
S31280
phytochrome - Martens's spike moss
C:Species: Selaginella martensii (Martens's spike moss)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: S31280; S25401
R:Hanelt, S.; Braun, B.; Marx, S.; Schneider-Poetsch, H.A.W.
Photochem. Photobiol. 55, 751-758, 1992
A:Title: Phytochrome evolution: a phylogenetic tree with the first complete seq
A:Reference number: S31280; MUID:93117303; PMID:1475321
A:Accession: S31280
A:Molecule type: DNA
A:Residues: 1-1134 <HAN>
A:Cross-references: UNIPROT:Q01549; UNIPARC:UPI0000131A4A; EMBL:X61458; NID:g222
A:Note: the authors translated the codon CTG for residue 239 as Arg, CAC for re
R:Schneider-Poetsch, H.A.W.; Braun, B.
Plant Physiol. 137, 576-580, 1991
A:Title: Proposal on the nature of phytochrome action based on the C-terminal s
A:Reference number: S25401
A:Accession: S25401
A:Molecule type: mRNA
A:Residues: '1', 730-899, 'GLHPP', 905-936, 'T', 938-1134 <SCH>

A;Cross-references: UNIPARC:UPI0000174E20
C;Genetics:
A;Introns: 686/1; 958/2; 1056/2
C;Superfamily: phytochrome, conventional type; phytochrome homology
F;Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
F;66-582/Domain: phytochrome homology <PHYT>
F;324/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 72.9%; Score 747; DB 2; Length 1134;
Best Local Similarity 67.9%; Pred. No. 1.5e-65;
Matches 142; Conservative 23; Mismatches 30; Indels 14; Gaps 2;

QY 1 KLAVALAISRLQSLPGDGIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVSEIRRSDL 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 203 KLAALAIISRLQSLPGDGIGLCTVVEEDVDVTGYDLWAYKFHEDEHGEVVAEIRRSDL 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 EPYLGLHYPATDIPQARFLFKQNRVMICDNCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 263 EPYLGLHYPATDIPQASRFLFMKNRVRMIDCSAPPVKITQDKELRQPISLAGSTLRAPH 322
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GCHTQYMANNGSVASIALAIVVKGK-----SSKLWGLVVGHHCSPRYVPFP 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 323 GCHTQYMANNGSVASLVAMIIINDNDPEPSGGGGGGGQHKGRRLWGLVVCCHTSPRSVFP- 381
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 168 LRYACEFLMQAFGLQQLQMLQSLAQLAEK 196
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 382 LRSACEFLMQVGLQLNMEAAVAHVREK 410
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
T09496
phytochrome - Douglas fir (fragment)
C;Species: Pseudotsuga menziesii (Douglas fir)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C;Accession: T09496
R;Marshall, K.A.; Neale, D.B.
submitted to the EMBL Data Library, March 1995
A;Reference number: Z16697
A;Accession: T09496
A;Status: preliminary; translated from GE/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-368 <MAR>
A;Cross-references: UNIPROT:Q04917; UNIPARC:UPI00000A3684; EMBL:U22458; NID:g726314; PID
C;Superfamily: phytochrome, conventional type; phytochrome homology
F;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;244/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 72.9%; Score 746; DB 2; Length 368;
Best Local Similarity 66.8%; Pred. No. 5e-66;
Matches 139; Conservative 22; Mismatches 35; Indels 12; Gaps 1;

QY 1 KLAVALAISRLQSLPGDGIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVSEIRRSDL 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 KLAALAIISRLQSLPGDGIGLCTVVEEDVDVTGYDLWAYKFHEDEHGEVVAEIRRSDL 182
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 EPYLGLHYPATDIPQARFLFKQNRVMICDNCNATPVKVVQSEELKRPCLCLVNSTLRAPH 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 183 EPYLGLHYPATDIPQASRFLFMKNRVRMIDCSAPPVKITQDKELRQPISLAGSTLRAPH 242
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GCHTQYMANNGSVASIALAIVVKGKSS-----KLWGLVVGHHCSPRYVPFP 168
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 243 GCHTQYMANNGSVASLVAMVVVTEKEEDADSEGGIQKGRRLWGLVVCCHTSPRYVPFP 302
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 169 RYACEFLMQAFGLQQLQMLQSLAQLAEK 196
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 RYACEFLMQVGLQLNMEAAVAHVREK 410
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: December 16, 2005, 15:30:17
Job time : 9.58967 secs